AMENDMENTS TO THE SPECIFICATION

Please amend the two paragraphs beginning on page 27, line 30, as follows:

- Figure 5 (A): comparison of the prediction of the secondary structure of the D4 (SEQ ID NO: 3) and D24 (SEQ ID NO: 7) aptamers. The secondary structure prediction is carried out using the RNA structure software written by David H. Mathews, ~~http://~~ rna.chem.rochester.edu. The algorithm is based on the searches described in D.H. Mathews et al. (Journal of Molecular Biology, 1999, 288, 911-940, mentioned above).

The same predictions can be obtained using the **mfold** algorithm, available on the site ~~http://~~bioinfo.math.rpi.edu/~zukerm/. The latter algorithm is based on the searches described in the publication in the name of D.H. Mathews et al., mentioned above. The consensus structure is in bold characters. (B): curve of binding of the D4 aptamer with PC12 MEN 2A cells; the D4 aptamer is radiolabeled with ^{32}P and incubated at various concentrations with cell monolayers. After several washes, the bound aptamer is quantified. The background noise is taken into account by subtracting, for each point obtained, the value obtained with a destructured D4 aptamer (D4Sc) having a scrambled sequence (*i.e.*, containing the same nucleotides, but in a different order). A Scatchard analysis (insert) is used to evaluate the binding constant and the number of targets.

Please insert the following paragraph before line 3 on page 4 of the specification (beneath the Table):

Sequence Codes D14 through D4 shown above respectively correspond to SEQ ID NOS: 3 to 15.